



6576608

1 CGCGGGGTGT TCTGGTGTCC CCCGCCCGC CTCTCCAAA AGCTACACCG ACGCGGACCG
GCGCCCCACA AGACCACAGG GGGCGGGGCG GAGAGGTTTT TCGATGTGGC TGCGCCTGGC

ssrI

61 CGGCGGCGTC CTCCCTCGCC CTCGCTTCAC CTCGCGGGCT CCGAATGCGG GGAGCTCGGA
GCCGCCGAG GAGGGAGCGG GAGCGAAGTG GAGCGCCCGA GGCTTACGCC CCTCGAGCCT

121 TGTCCGGTTT CCTGTGAGGC TTTTACCTGA CACCCGCCGC CTTTCCCCGG CACTGGCTGG
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kasI

181 GAGGGCGCCC TGCAAAGTTG GGAACGCGGA GCCCGGACC CGCTCCCGCC GCCTCCGGCT
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241 CGCCAGGGG GGGTCGCCG GAGGAGCCCG GGGGAGAGGG ACCAGGAGGG GCCCGCGGCC
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kasI

ageI

301 TCGCAGGGGC GCCCGCGCCC CCACCCCTGC CCCCGCCAGC GGACCGGTCC CCCACCCCCG
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361 GTCCTTCCAC CATGCACTTG CTGGGCTTCT TCTCTGTGGC GTGTTCTCTG CTCGCCGCTG
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-20 M H L L G F F S V A C S L L A A A

kasI

421 CGCTGCTCCC GGGTCTCGC GAGGCGCCCG CCGCCGCCGC CGCCTTCGAG TCCGGACTCG
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-3 L L P G P R E A P A A A A A F E S G L D

481 ACCTCTCGGA CGCGGAGCCC GACGCGGGCG AGGCCACGGC TTATGCAAGC AAAGATCTGG
TGGAGAGCCT GCGCCTCGGG CTGCGCCCGC TCCGGTGCCG AATACGTTCT TTTCTAGACC

18 L S D A E P D A G E A T A Y A S K D L E

541 AGGAGCAGTT ACGGTCTGTG TCCAGTGTAG ATGAACTCAT GACTGTACTC TACCCAGAAT
TCCTCGTCAA TGCCAGACAC AGGTCACATC TACTTGAGTA CTGACATGAG ATGGGTCTTA

38 E Q L R S V S S V D E L M T V L Y P E Y

FIG. 1A



601 ATTGGAAAAT GTACAAGTGT CAGCTAAGGA AAGGAGGCTG GCAACATAAC AGAGAACAGG
TAACCTTTTA CATGTTTACA GTCGATTCTT TTCCTCCGAC CGTTGTATTG TCTCTTGTCC
58 W K M Y K C Q L R K G G W Q H N R E Q A

661 CCAACCTCAA CTCAAGGACA GAAGAGACTA TAAAATTTGC TGCAGCACAT TATAATACAG
GGTTGGAGTT GAGTTCCTGT CTTCTCTGAT ATTTTAAACG ACGTCGTGTA ATATTATGTC
78 N L N S R T E E T I K F A A A H Y N T E

sphI

721 AGATCTTGAA AAGTATTGAT AATGAGTGGA GAAAGACTCA ATGCATGCCA CGGGAGGTGT
TCTAGAACTT TTCATACTA TTACTCACCT CTTTCTGAGT TACGTACGGT GCCCTCCACA
98 I L K S I D N E W R K T Q C M P R E V C

781 GTATAGATGT GGGGAAGGAG TTTGGAGTCG CGACAAACAC CTTCTTTAAA CCTCCATGTG
CATATCTACA CCCCTTCCTC AAACCTCAGC GCTGTTTGTG GAAGAAATTT GGAGGTACAC
118 I D V G K E F G V A T N T F F K P P C V

accI

841 TGTCCGTCTA CAGATGTGGG GGTGCTGCA ATAGTGAGGG GCTGCAGTGC ATGAACACCA
ACAGGCAGAT GTCTACACCC CCAACGACGT TATCACTCCC CGACGTCACG TACTTGTGGT
138 S V Y R C G G C C N S E G L Q C M N T S

901 GCACGAGCTA CCTCAGCAAG ACGTTATTTG AAATTACAGT GCCTCTCTCT CAAGGCCCCA
CGTGCTCGAT GGAGTCGTTT TGCAATAAAC TTTAATGTCA CGGAGAGAGA GTTCCGGGGT
158 T S Y L S K T L F E I T V P L S Q G P K

961 AACCAGTAAC AATCAGTTTT GCCAATCACA CTTCTGCGG ATGCATGTCT AACTGGATG
TTGGTCATTG TTAGTCAAAA CGGTTAGTGT GAAGGACGGC TACGTACAGA TTTGACCTAC
178 P V T I S F A N H T S C R C M S K L D V

1021 TTTACAGACA AGTTCATTCC ATTATTAGAC GTTCCCTGCC AGCAACACTA CCACAGTGTC
AAATGTCTGT TCAAGTAAGG TAATAATCTG CAAGGGACGG TCGTTGTGAT GGTGTCACAG
198 Y R Q V H S I I R R S L P A T L P Q C Q

1081 AGGCAGCGAA CAAGACCTGC CCCACCAATT ACATGTGGAA TAATCACATC TGCAGATGCC
TCCGTCGCTT GTTCTGGACG GGGTGGTTAA TGTACACCTT ATTAGTGTAG ACGTCTACGG
218 A A N K T C P T N Y M W N N H I C R C L

FIG. 1B



1141 TGGCTCAGGA AGATTTTATG TTTTCCTCGG ATGCTGGAGA TGA CTCAACA GATGGATTCC
ACCGAGTCCT TCTAAAATAC AAAAGGAGCC TACGACCTCT ACTGAGTTGT CTACCTAAGG
238 A Q E D F M F S S D A G D D S T D G F H

1201 ATGACATCTG TGGACCAAAC AAGGAGCTGG ATGAAGAGAC CTGTCA GTGT GTCTGCAGAG
TACTGTAGAC ACCTGGTTTG TTCCTCGACC TACTTCTCTG GACAGTCACA CAGACGTCTC
258 D I C G P N K E L D E E T C Q C V C R A

1261 CGGGGCTTCG GCCTGCCAGC TGTGGACCCC ACAAAGAACT AGACAGAAAC TCATGCCAGT
GCCCCGAAGC CGGACGGTCG ACACCTGGGG TGTTTCTTGA TCTGTCTTTG AGTACGGTCA
278 G L R P A S C G P H K E L D R N S C Q C

1321 GTGTCTGTAA AAACAAACTC TTCCCCAGCC AATGTGGGGC CAACCGAGAA TTTGATGAAA
CACAGACATT TTTGTTTGAG AAGGGGTCGG TTACACCCCG GTTGGCTCTT AAAC TACTTT
298 V C K N K L F P S Q C G A N R E F D E N

1381 ACACATGCCA GTGTGTATGT AAAAGAACCT GCCCCAGAAA TCAACCCCTA AATCCTGGAA
TGTGTACGGT CACACATACA TTTTCTTGGA CGGGGTCTTT AGTTGGGGAT TTAGGACCTT
318 T C Q C V C K R T C P R N Q P L N P G K

1441 AATGTGCCTG TGAATGTACA GAAAGTCCAC AGAAATGCTT GTTAAAAGGA AAGAAGTTCC
TTACACGGAC ACTTACATGT CTTTCAGGTG TCTTTACGAA CAATTTTCCT TTCTTCAAGG
338 C A C E C T E S P Q K C L L K G K K F H

ea eI

1501 ACCACCAAAC ATGCAGCTGT TACAGACGGC CATGTACGAA CCGCCAGAAG GCTTGTGAGC
TGGTGGTTTG TACGTCGACA ATGTCTGCCG GTACATGCTT GGCGGTCTTC CGAACACTCG
358 H Q T C S C Y R R P C T N R Q K A C E P

1561 CAGGATTTTC ATATAGTGAA GAAGTGTGTC GTTGTGTCCC TTCATATTGG AAAAGACCAC
GTCCTAAAAG TATATCACTT CTTACACAG CAACACAGGG AAGTATAACC TTTTCTGGTG
378 G F S Y S E E V C R C V P S Y W K R P Q

cl aI

1621 AAATGAGCTA AGATTGTACT GTTTTCCAGT TCATCGATTT TCTATTATGG AAAACTGTGT
TTTACTCGAT TCTAACATGA CAAAAGGTCA AGTAGCTAAA AGATAATACC TTTTGACACA
398 M S O

1681 TGCCACAGTA GAACTGTCTG TGAACAGAGA GACCCTTGTG GGTCCATGCT AACAAAGACA
ACGGTGT CAT CTTGACAGAC ACTTGTCTCT CTGGGAACAC CCAGGTACGA TTGTTTCTGT

FIG. 1C



Inventor: LEE ET AL.
Docket No.: 9.111USD1
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estI

1741 AAAGTCTGTC TTTCCTGAAC CATGTGGATA ACTTTACAGA AATGGACTGG AGCTCATCTG
TTTCAGACAG AAAGGACTTG GTACACCTAT TGAAATGTCT TTACCTGACC TCGAGTAGAC

1801 CAAAAGGCCT CTTGTAAAGA CTGGTTTTCT GCCAATGACC AAACAGCCAA GATTTTCCTC
GTTTTCCGGA GAACATTTCT GACCAAAAGA CGGTTACTGG TTTGTCGGTT CTAAAAGGAG

1861 TTGTGATTTT TTTAAAAGAA TGACTATATA ATTTATTTCC ACTAAAATA TTGTTTCTGC
AACACTAAAG AAATTTTCTT ACTGATATAT TAAATAAAGG TGATTTTTAT AACAAAGACG

1921 ATTCATTTTT ATAGCAACAA CAATTGGTAA AACTCACTGT GATCAATATT TTTATATCAT
TAAGTAAAAA TATCGTTGTT GTTAACCATT TTGAGTGACA CTAGTTATAA AAATATAGTA

1981 GCAAAATATG TTTAAAATAA AATGAAAATT GTATTAAAAA AAAAAAAAAA A
CGTTTTATAC AAATTTTATT TTAATTTTAA CATAATTTTT TTTTTTTTTT T

FIG. 1D



Inventor: LEE ET AL.
Docket No.: 669.111USD1
Title: METHODS OF USING VEGF-RELATED PROTEIN
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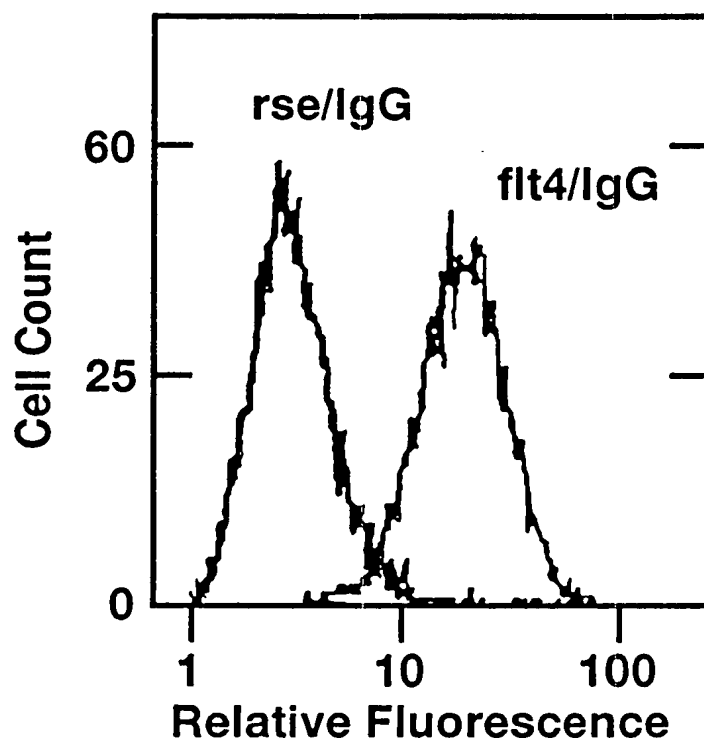


FIG. 2

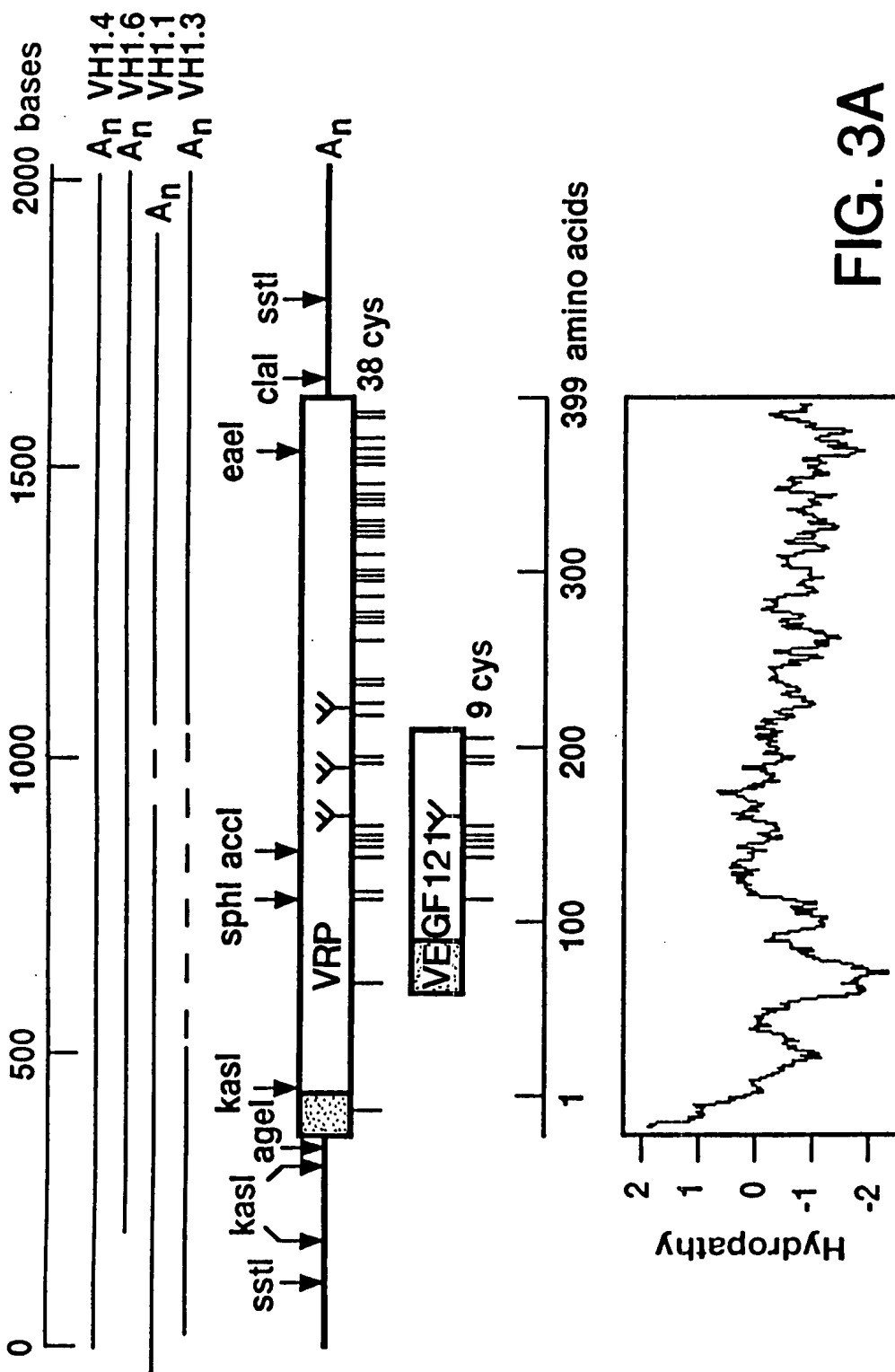


FIG. 3A



VRP -20 MHLGFFSVACSLAAALLPGPREAPAAAASFESGLDLSDAEPDAGEATA
VRP 31 YASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCKQLRKGGWQHNRREQANLN
VEGF121 -26 MNFLLSWVHWSLA LLYLHHA
PIGF131 -18 MPVMR LFPCLQL LAGLALPA
VRP 81 SRTEETIKFAAHYNTEILKSIDNEWRKTQCMPREVCIDVVGKEFGVATNT
VEGF121 -5 KWSQAAPMAEGGQNHHHEVVVFMDVYQRSYCHPIETLVDFIQEYPDIEIY
PIGF131 4 VPPQQWALSAGNGSSSEVEVVPEEQEVWGRSYCRALERLVDVVVS EYPS EIVEH
VRP 131 FFKPPCVSVYRCGGGCCNS EGLQCMNTSTSYLSKTLFEITVPLSQGPKPVT
VEGF121 46 IFKPSCVP LMRGCGGCCNDEGLECVPTESNITMQIMRIKP--HQQQHIGE
PIGF131 54 MFSPPSCVSL LRCRTGCCGDENLHCVPVETANVTMQLIKILRS--GDRP S YVE
VRP 181 ISFANHTSCRCMSKL DVYRQVHS IIRSLPATLPQCQAANKTCPTNYMWN
VEGF121 94 MSFLQHNNKCECRPKKDRARQEKCDKPRR
PIGF131 102 LTESQHVRCECRPLREKMKPERCGDAVPRR
VRP 231 NHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLR
VRP 281 PASCGPHKELDRNSCQCVCCKNKLFPSCCGGANREFDENTCQCVCCKRTCPRN
VRP 331 QPLNPGKACECTESPQKCLLKGGKFHHQTCSCYRRPCTNRQKACEPGFS
VRP 381 YSEEVCRCPVSYWKR PQMS

FIG. 3B

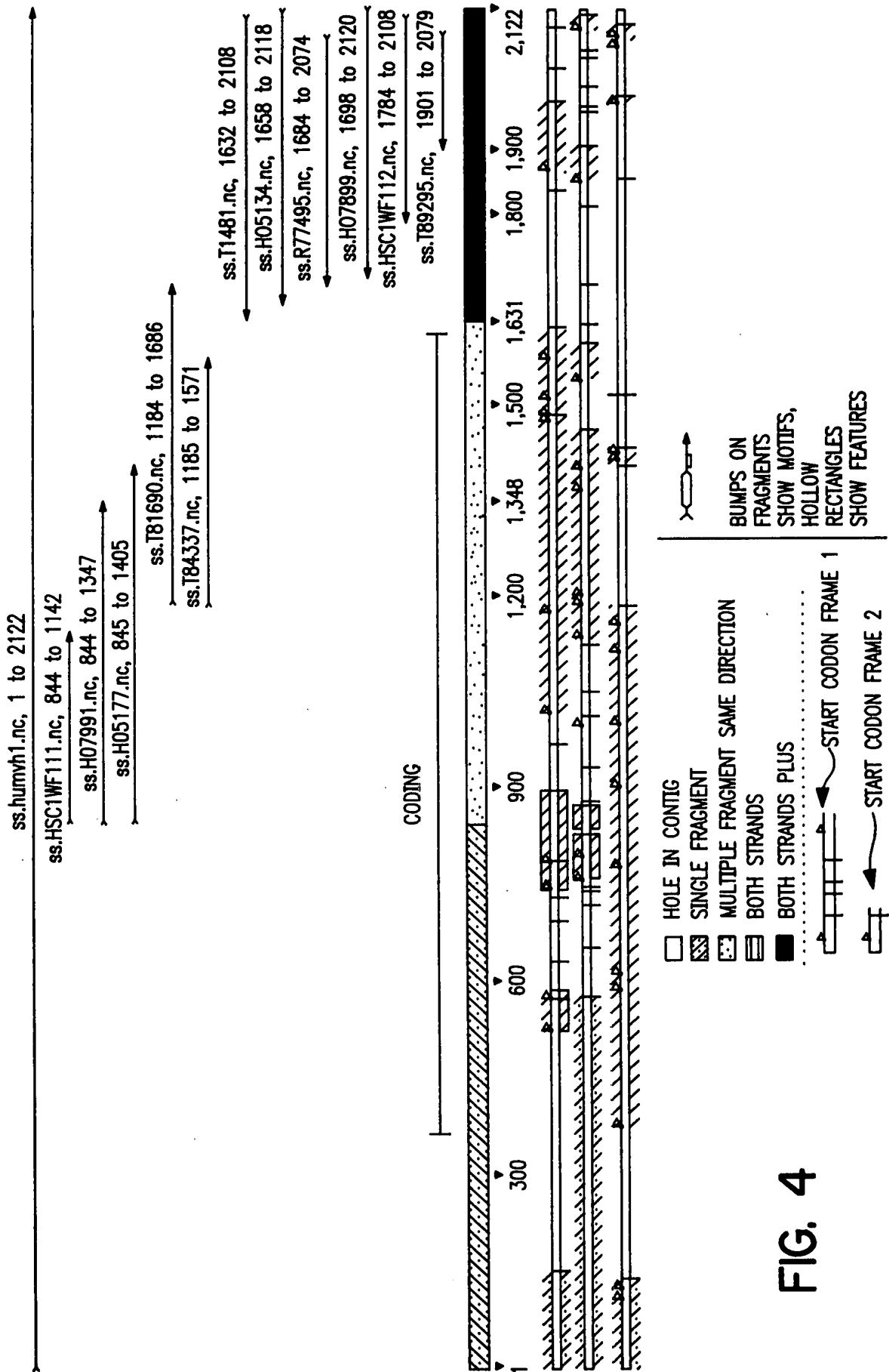


FIG. 4

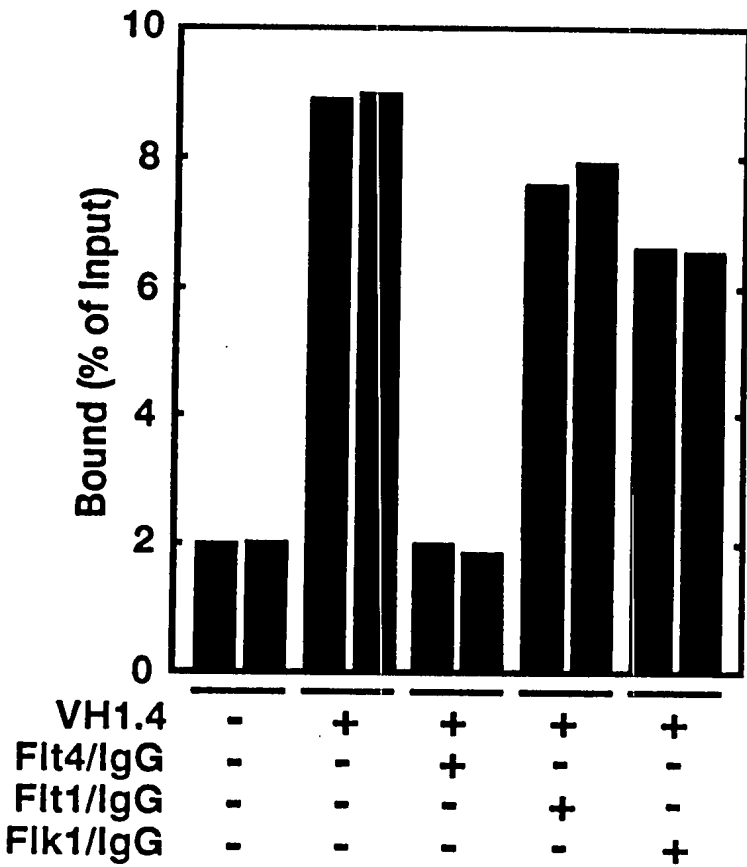


FIG. 5A

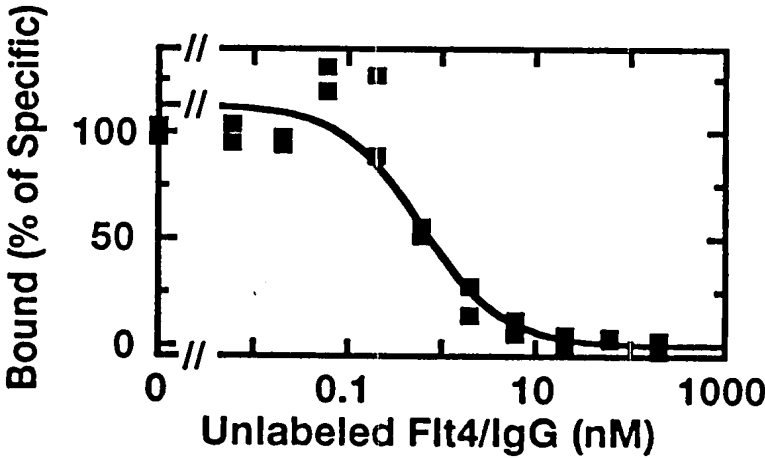


FIG. 5B

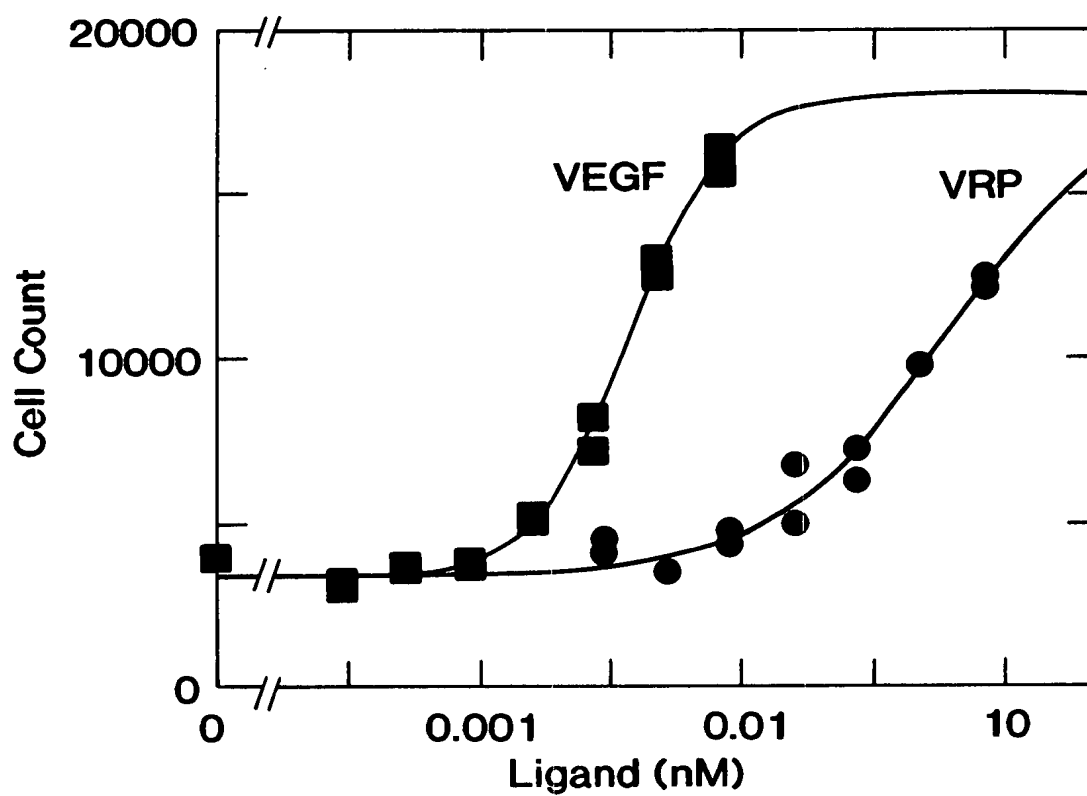
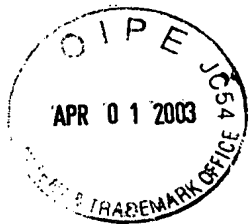


FIG. 6